

**FIG. 1**  
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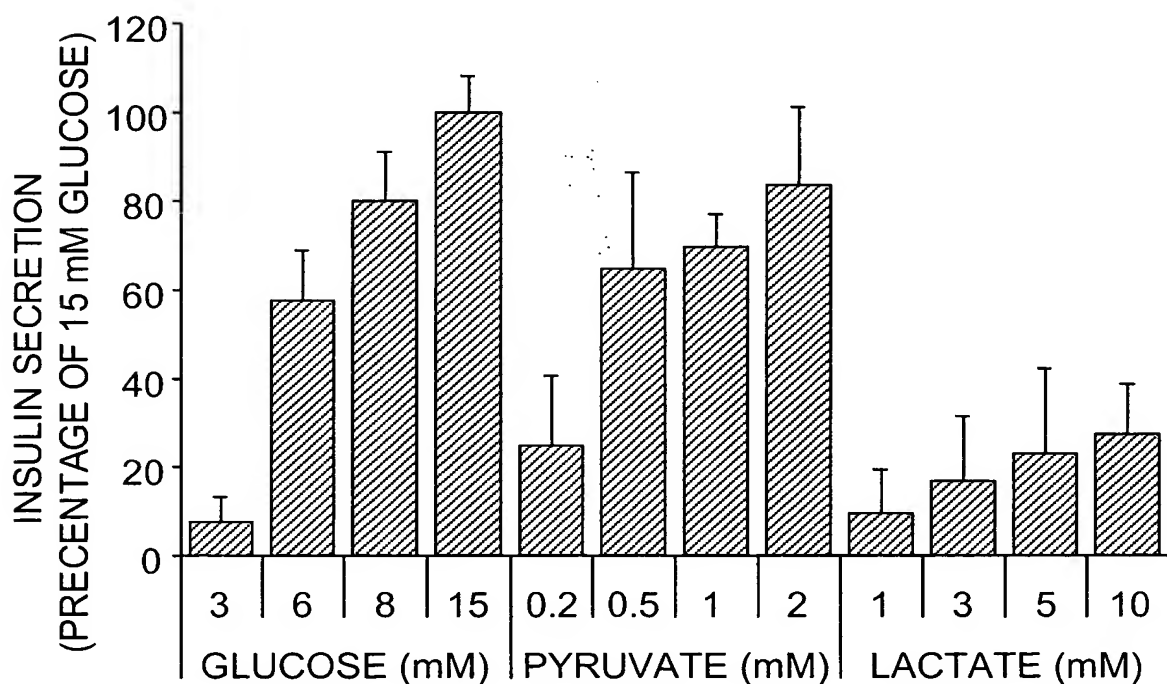
GTGTGCTGGA	GCCACTGTCTG	CCGATCTCGC	GCACGCTACT
GCTGCTGCTC	GCCCGTCTGTC	CCCCATCGTG	CACTAAGCGG
TCCCAAAGA	TTCAAAGTCC	AAG <b>AT</b> GGCAG	CCCTCAAGGA
CCAGCTGATT	GTGAATCTTC	TTAAGGAAGA	ACAGGTCCCC
CAGAACAGA	TTACAGTTGT	TGGGGTTGGT	GCTGTTGGCA
TGGCTTGTGC	CATCAGTATC	TTAATGAAGG	ACTTGGCTGA
TGAGCTTGCC	CTTGTTGATG	TCATAGAAGA	TAAGCTAAAG
GGAGAGATGA	TGGATCTTCA	GCATGGCAGC	CTTTTCCTTA
AGACACCAA	AATTGTCTCC	AGCAAAGATT	ATAGTGTGAC
TGCAAACCTC	AAGCTGGTCA	TTATCACCGC	GGGGGCCCGT
CAGCAAGAGG	GAGAGAGCCG	GCTCAATTTG	GTCCAGCGAA
ACGTGAACAT	CTTCAAGTTC	ATCATTCCAA	ATGTTGTGAA
ATACAGTCCA	CAGTGCAAAC	TGCTCATCGT	CTCAAACCCA
GTGGATATCT	TGACCTACGT	GGCTTGGAAG	ATCAGCGGCT
TCCCCAAAA	CAGAGTTATT	GGAAGTGGTT	GCAATCTGGA
TTCGGCTCGG	TTCCGTTACC	TGATGGGAGA	AAGGCTGGGA
GTTTCATCCAC	TGAGCTGTCA	CGGGTGGGTC	CTGGGAGAGC
ATGGCGACTC	CAGTGTGCCT	GTGTGGAGTG	GTGTGAACGT
CGCCGGCGTC	TCCCTGAAGT	CTCTGAACCC	GCAGCTGGGC
ACGGATGCAG	ACAAGGAGCA	GTGGAAGGAT	GTGCACAAGC
AGGTGGTTGA	CAGTGCATAC	GAAGTGATCA	AGCTGAAAGG
TTACACATCC	TGGGCCATTG	GCCTCTCCGT	GGCAGACTTG
GCCGAGAGCA	TAATGAAGAA	CCTTAGGCGG	GTGCATCCCA
TTTCCACCAT	GATTAAGGGT	CTCTATGGAA	TCAAGGAGGA
TGTCTTCCTC	AGCGTCCCAT	GTATCCTGGG	ACAAAATGGA
ATCTCAGATG	TTGTGAAGGT	GACACTGACT	CCTGACGAGG
AGGCCCGCCT	GAAGAAGAGT	GCAGATACCC	TCTGGGGAAT
CCAGAAGGAG	CTGCAGTTCT	<b>AA</b> AGTCTTCC	CAGTGTCCTA
GCACTTCACT	GTCCAGGCTG	CAGCAGGGTT	TCTATGGAGA
CCACGCACTT	CTCATCTGAG	CTGTGGTTAG	TCCAGTTGGT
CCAGTTGTGT	TGAGGTGGTC	TGGGGGAAAT	CTCAGTTCCA
CAGCTCTACC	CTGCTAAGTG	GTACTTGTGT	AGTGGTAACC
TGGTTAGTGT	GACAATCCCA	CTGTCTCCAA	GACACACTGC
CAACTGCATG	CAGGCTTTGA	TTACCCTGTG	AGCCTGCTGC
ATTGCTGTGC	TACGCACCCT	CACCAAACAT	GCCTAGGCCA
TGAGTTCCCA	GTTAGTTATA	AGCTGGCTCC	AGTGTGTAAAG
TCCATCGTGT	ATATCTTGTG	CATAAATGTT	CTACAGGATA
TTTTCTGTAT	TATATGTGTC	TGTAGTGTAC	ATTGCAATAT
TACGTGAAAT	GTAAGATCTG	CATATGGATG	ATGGAACCAA
CCACTCAAGT	GTCATGCCAA	GGAAAACACC	AAATAAACCT
TGAACAGTG			

**FIG. 2A**

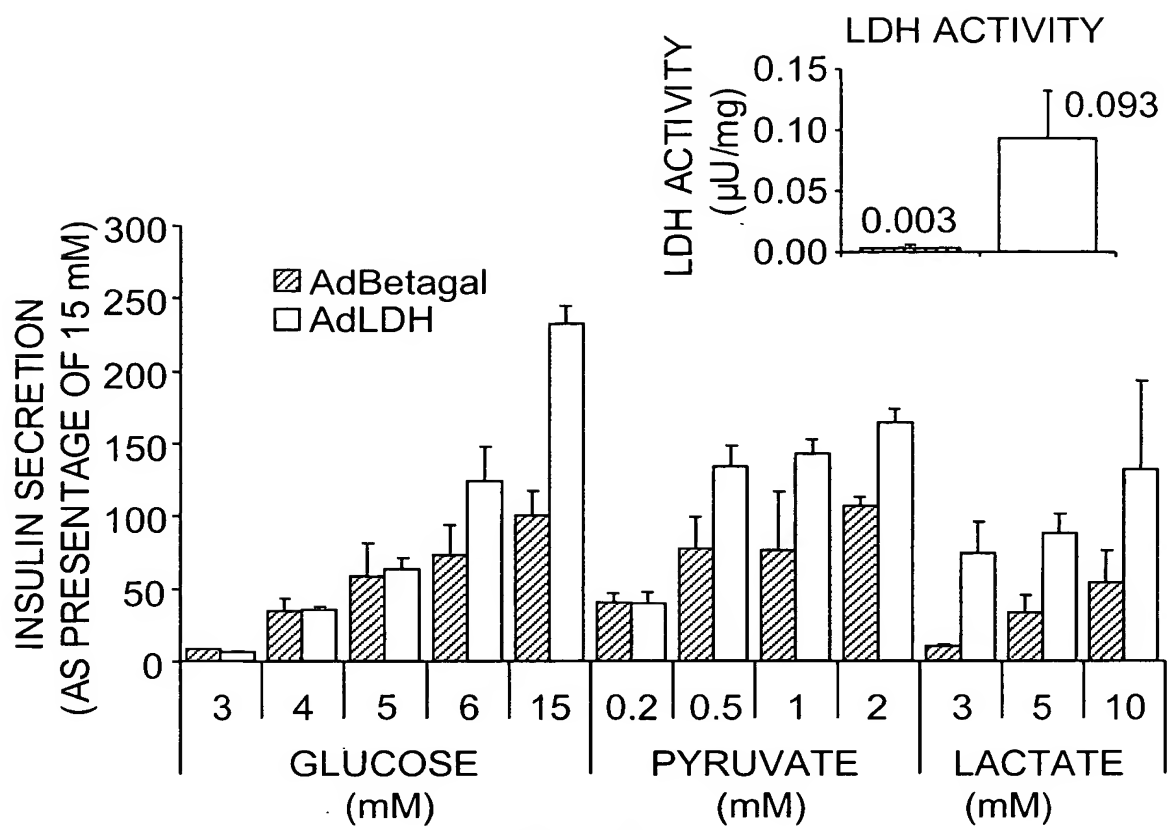
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MAALKDQLIVNLLKEEQVPQNKITVVGVGAVGMACAISILMKDLADEL  
 ALVDVIEDKCLKGEMMDLQHGSFLKTPKIVSSKDYSVTANSKLVIIITA  
 GARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPQCKLLIVSNPVDILT  
 YVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWVLGE  
 HGDSSVPVWSGVNVAGVSLKSLNPQLGTDADKEQWKDVHKQVVDSAYE  
 VIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGIKEDVF  
 LSVPCILGQNGISDVVKVTLTPDEEARLKKSADTLWGIQKELQF

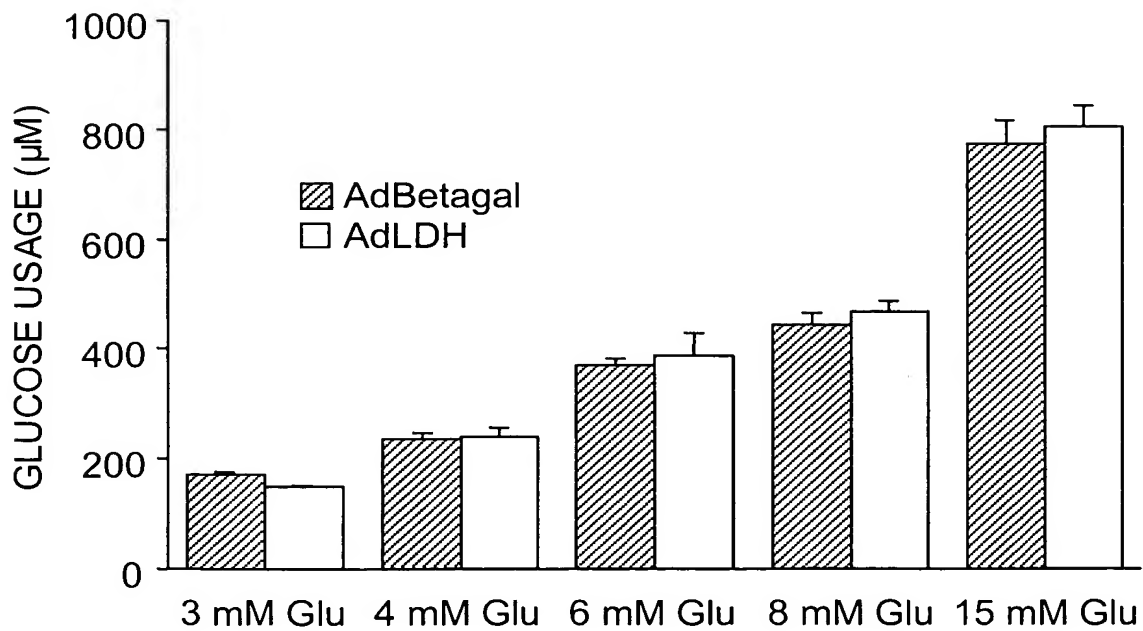
*FIG. 2B*



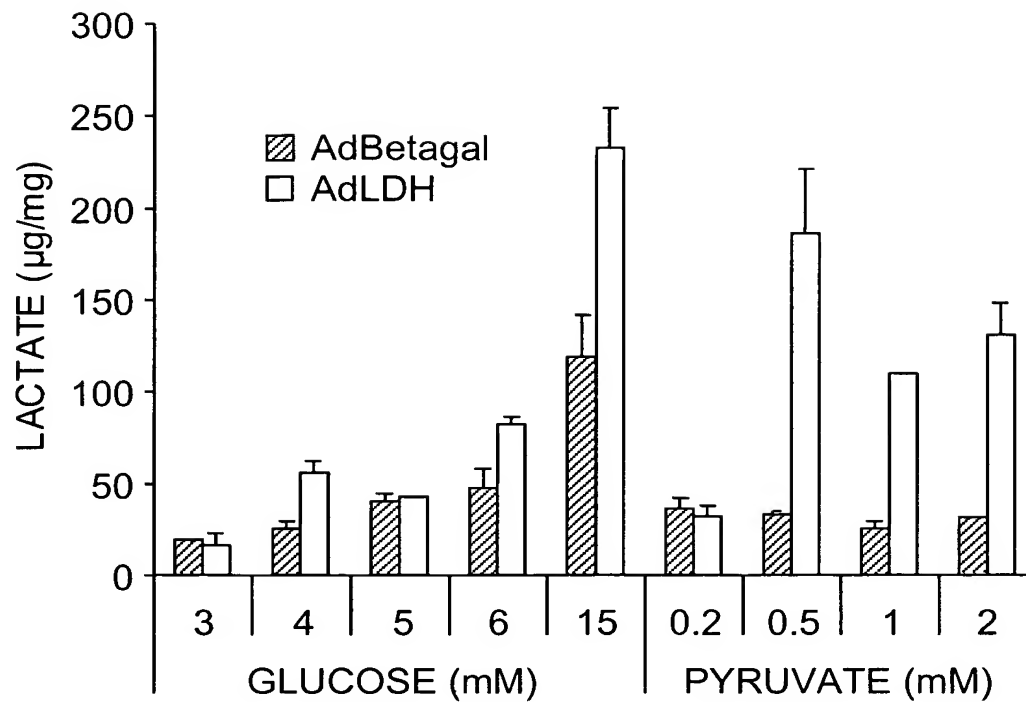
*FIG. 3*



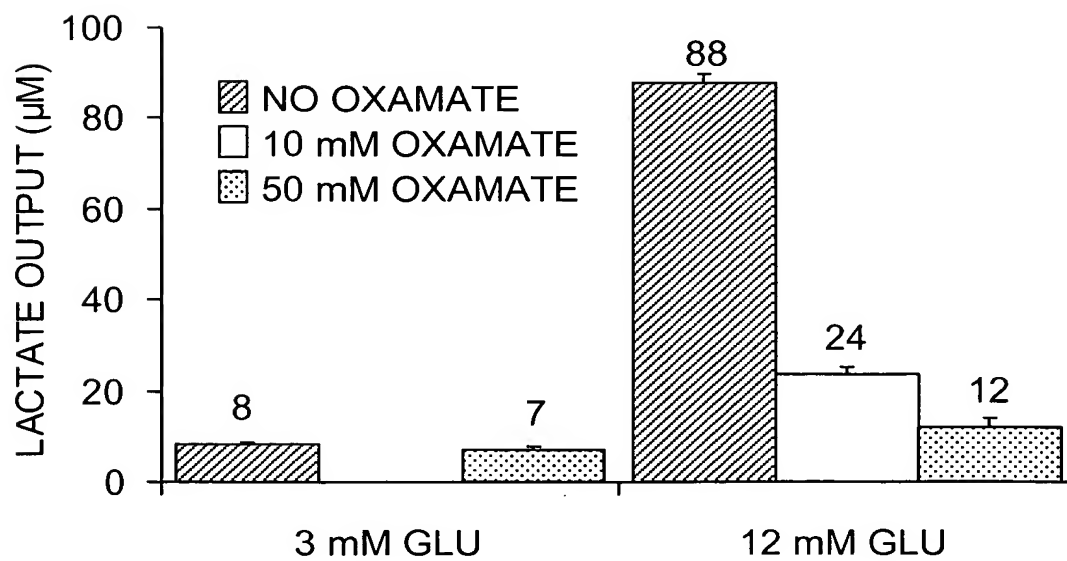
**FIG. 4**



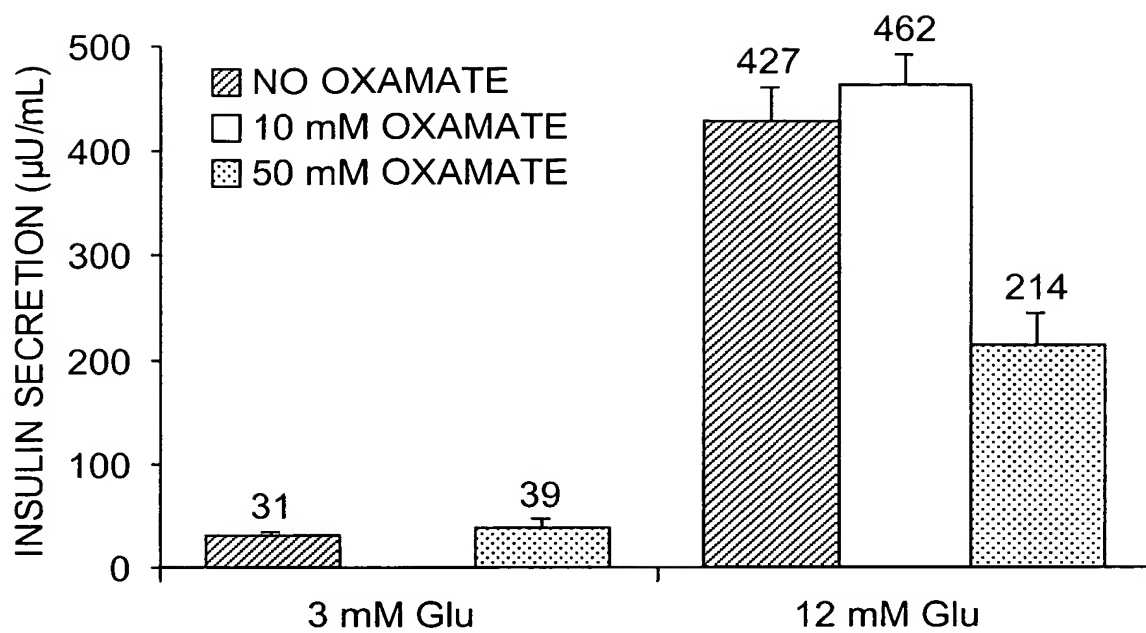
**FIG. 5**



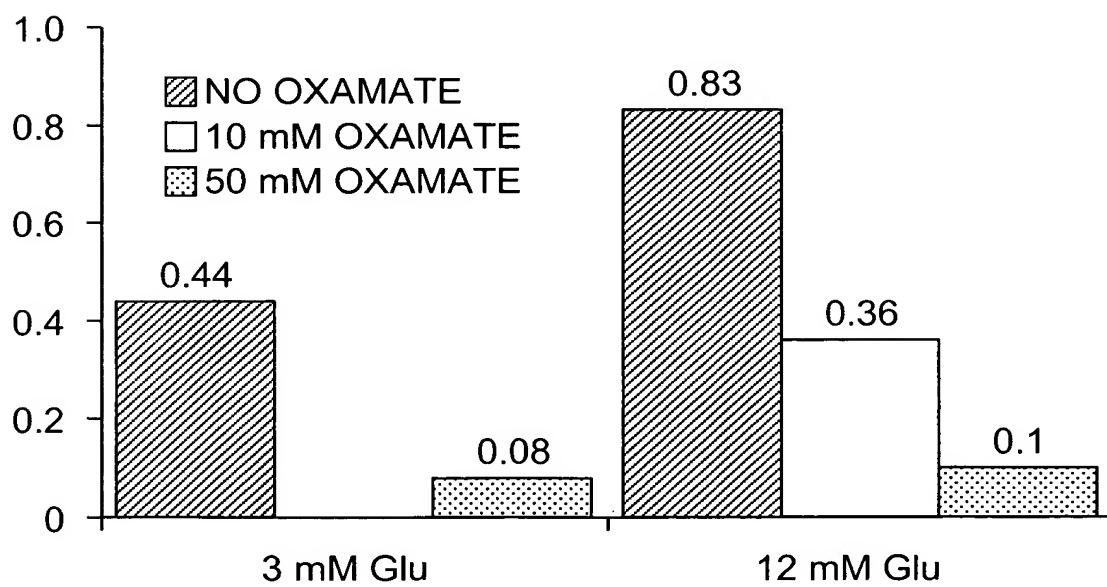
**FIG. 6**



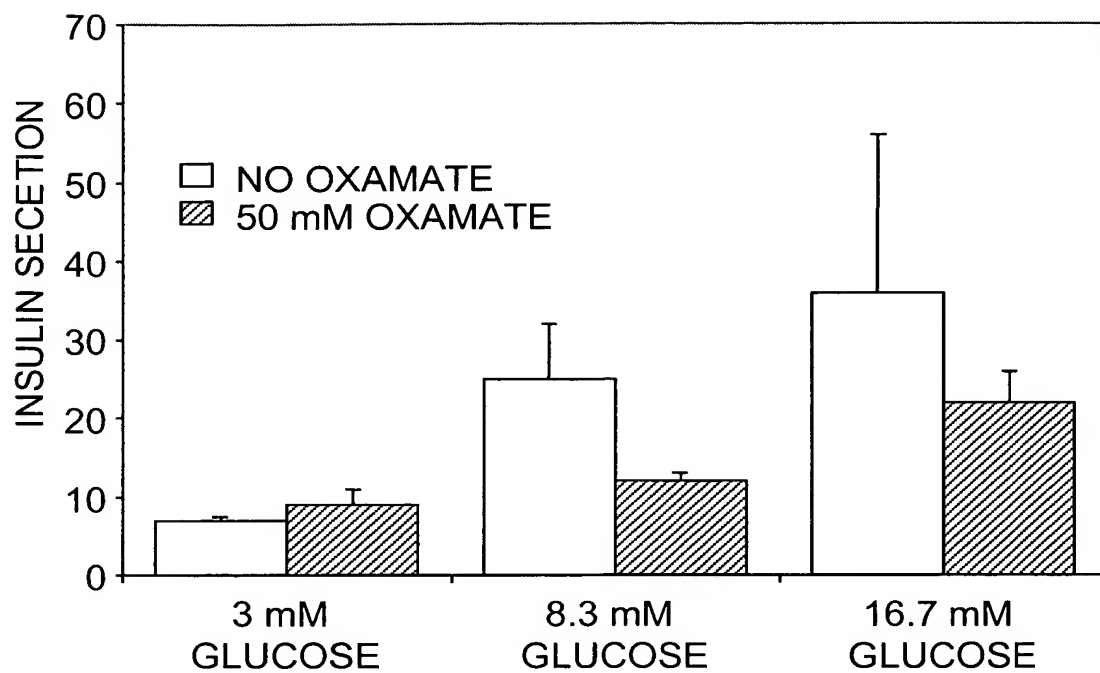
**FIG. 7**



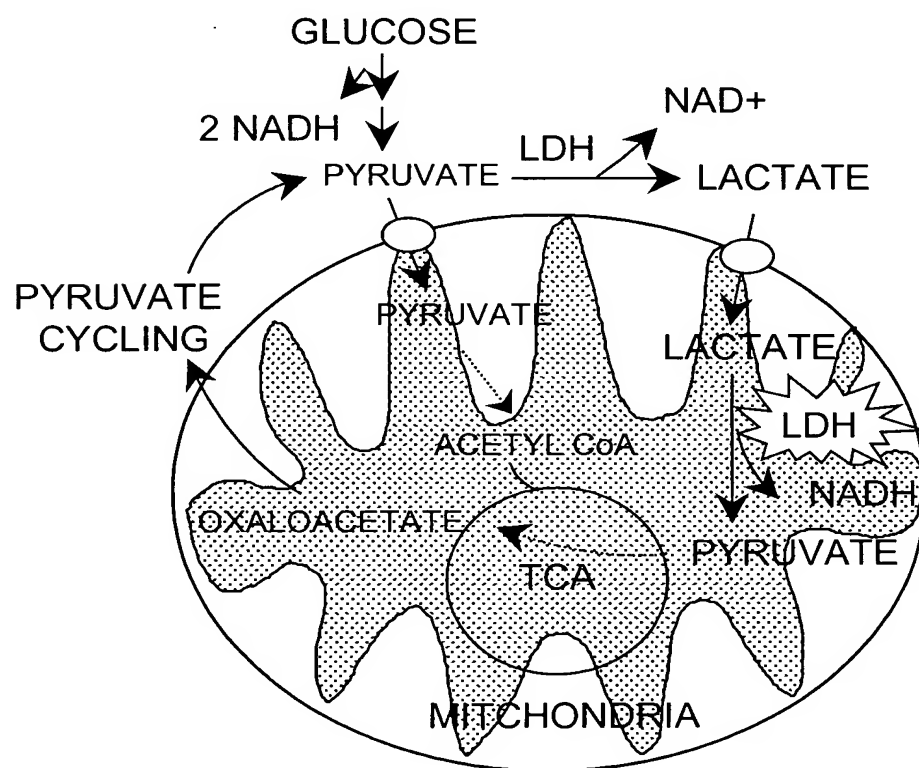
*FIG. 7B*



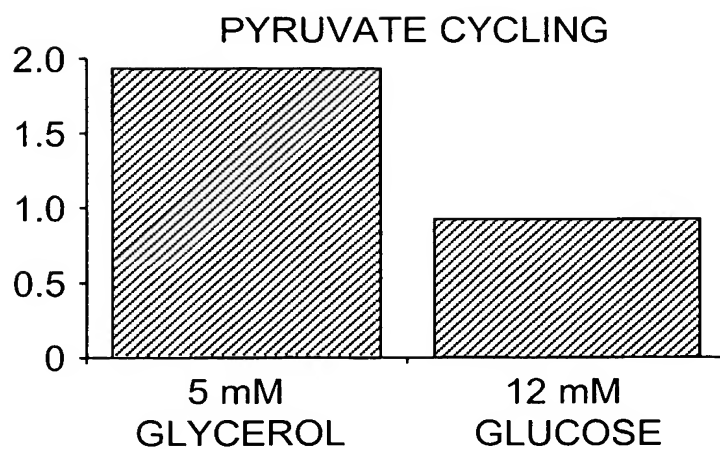
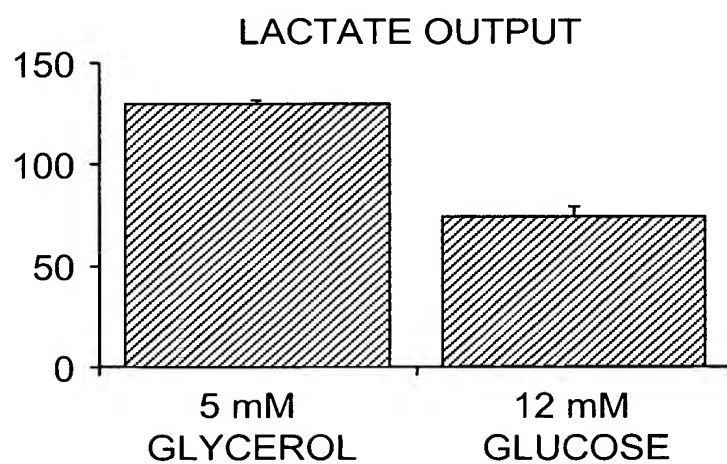
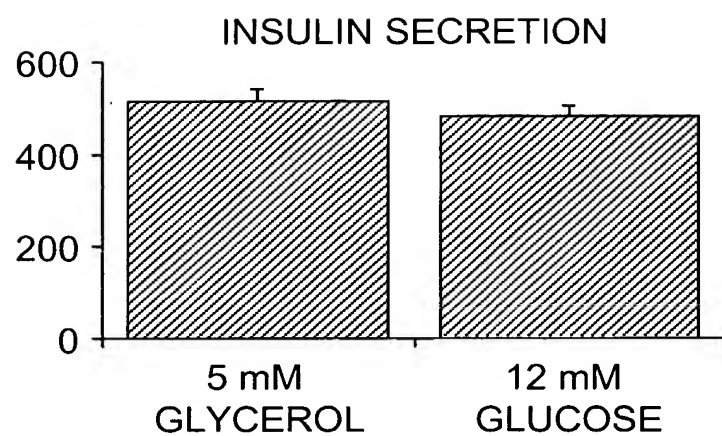
*FIG. 7C*



**FIG. 7D**



**FIG. 8**



**FIG. 9**  
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• RAT     MSKNSGGYTYTETSVLFFHF~~K~~VPKDSKSK  
 • MOUSE MSKSSGGYTYTETSVLFFHF~~K~~VSKDSKSK  
 • HUMAN MGEPSGGYTYTQTSIFLFHAKIPFGSKSN

• CONS    MSK SGGYTYTETSVLFFHF~~K~~VPKDSKSK

## FIG. 11

CGCTCTACTT GCTGTAGGAC TCTGGGTGAT GGGAGAAGAG CGGGAGGGCA

GTTCTTTAAC CGTGTAAGAG GAGGGACCAT CCCTTTTGGG GTTCATCAAG  
ATGAGTAAGA ACTCAGGCGG CTACACATAT ACGGAGACCT CAGTATTATT  
 \*\*\*

TTTCCATTTT AAGGTCCCAA AAGATTCAAA GTCCAAGATG GCAGCCCTCA  
 \$\$\$

AGGACCAGCT GATTGTGAAT CTTCTTAAGG AAGAACAGGT CCCCAGAAC  
 AAGATTACAG TTGTTGGGGT TGGTGCTGTT GGCATGGCTT GTGCCATCAG  
 TATCTTAATG AAGGACTTGG CTGATGAGCT TGCCCTTGTT GATGTCATAG  
 AAGATAAGCT AAAGGGAGAG ATGATGGATC TTCAGCATGG CAGCCTTTTC  
 CTTAAGACAC CAAAAATTGT CTCCAGCAAA GATTATAGTG TGACTGCAAA  
 CTCCAAGCTG GTCATTATCA CCGCGGGGGC CCGTCAGCAA GAGGGAGAGA  
 GCCGGCTCAA TTTGGTCCAG CGAAACGTGA ACATCTTCAA GTTCATCATT  
 CCAAATGTTG TGAAATACAG TCCACAGTGC AAAGTGCTCA TCGTCTCAAA  
 CCCAGTGGAT ATCTTGACCT ACGTGGCTTG GAAGATCAGC GGCTTCCCCA  
 AAAACAAAGT TATTGGAAGT GGTGCAATC TGGATTCGGC TCGGTTCCGT  
 TACCTGATGG GAGAAAGGCT GGGAGTTTAT CCACTGAGCT GTCACGGGTG  
 GGTCCTGGGA GAGCATGGCG ACTCCAGTGT GCCTGTGTGG AGTGGTGTGA  
 ACGTCGCCGG CGTCTCCCTG AAGTCTCTGA ACCCGCAGCT GGGCACGGAT  
 GCAGACAAGG AGCAGTGGAA GGATGTGCAC AAGCAGGTGG TTGACAGTGC  
 ATACGAAGTG ATCAAGCTGA AAGGTACAC ATCCTGGGCC ATTGGCCTCT  
 CCGTGGCAGA CTTGGCCGAG AGCATAATGA AGAACCTTAG GCGGGTGCAT  
 CCCATTTCCA CCATGATTAA GGGTCTCTAT GGGATCAAGG AGGATGTCTT  
 CCTCAGCGTC CCATGTATCC TGGGACAAAA TGAATCTCA GATGTTGTGA  
 AGGTGACACT GACTCCTGAC GAGGAGGCC GCCTGAAGAA GAGTGCAGAT  
 ACCCTCTGGG GAATCCAGAA GGAGCTGCAG TTCTAAAGTC TTCCAGTGT  
CCTAGCACTT CACTGTCCAG GCTGCAGCAG GGTTCCTATG GAGACCACGC  
ACTTCTCATC TGAGCTGTGG TTAGTCCAGT TGGTCCA

- \* MITOCHONDRIAL START SITE
- \$ CYTOSOLIC START SITE
- OVERLINED 5' ORF
- PRIMER SEQUENCES ARE UNDERLINED

## FIG. 12A

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MSKNSGGYTYTETSVLFFHFKVPKDSKSKMAALKDQLIVNLLKEEQVPQ  
NKITVVGVGAVGMACAISILMKDLADELALVDVIEDKCLKGEMMDLQHGS  
LFLKTPKIVSSKDYSVTANSKLVIITAGARQQEGESRLNLVQRNVNIFK  
FIIPNVVKYSPQCKLLIVSNPVDILTIVAWKISGFPKNRVIGSGCNLDS  
ARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLKSLNP  
QLGTDADKEQWKDVHKQVVD SAYEVIKCLKGYTSWAIGLSVADLAESIMK  
NLRRVHPISTMIKGLYGIKEDVFLSVPCILGQNGISDVVKVTLTPDEEA  
RLKKSADTLWGIQKELQF

*FIG. 12B*

GAGCAACTTGGCGCTCTACTTGCTGTAGGGCTCTGGGTGATGGGAGAAGAGCGGGAG  
GGCAGCTTTCTAACCATAAAGAGGAGATAACCATCCCCCTTTGGTTCATCAAG ATGA  
GTAAGTCCTCAGGCGGCTACACGTACACGGAGACCTCGGTATTATTTTCCATTTCA  
AGGTCTCAAAGATTCAAAGTCCAAGATGGCAACCTCAAGGACCAGCTGATTGTGA  
ATCTTCTTAAGGAAGAGCAGGCTCCCCAGAACAAGATTACAGTTGTTGGGGTTGGTG  
CTGTTGGCATGGCTTGTGCCATCAGTATCTTAATGAAGGACTTGGCGGATGAGCTTG  
CCCTTGTTGACGTCATGGAAGACAACTCAAGGGCGAGATGATGGATCTCCAGCATG  
GCAGCCTCTTCCTTAAACACCAAAAATTGTCTCCAGCAAAGACTACTGTGTAAGT  
CGAACTCCAAGCTGGTCATTATCACCGCGGGGGGCCGTCAGCAAAGAGGGGGAGAGCC  
GGCTCAACCTGGTCCAGCGAAACGTGAACATCTTCAAGTTCATCATTCCCAACATTG  
TCAAGTACAGTCCACACTGCAAGCTGCTGATCGTCTCCAATCCAGTGGATATCTTGA  
CCTACGTGGCTTGGAAAATCAGTGGCTTTCCCAAAAACCGAGTAATTGGAAGTGGTT  
GCAATCTGGATTACAGCGCGGTTCCGTTACCTGATGGGAGAGAGGCTGGGGGTTACG  
CGCTGAGCTGTCACGGCTGGGTCTTGGGAGAACATGGCGACTCCAGTGTGCCTGTGT  
GGAGTGGTGTGAATGTTGCCGGCGTCTCCCTGAAGTCTCTTAACCCAGAACTGGGCA  
CTGACGCAGACAAGGAGCAGTGGAAAGGAGGTTCAACAAGCAGGTGGTGGACAGTGCCT  
ACGAGGTGATCAAGCTGAAAGGTTACACATCCTGGGCCATTGGCCTCTCTGTGGCAG  
ACTTGGCTGAGAGCATAATGAAGAACCTTAGGCGGGTGCATCCCATTTCACCATGA  
TTAAGGGTCTCTATGGAATCAATGAGGATGTCTTCTCAGTGTCCCATGTATCCTGG  
GACAAAATGGAATCTCGGATGTTGTGAAGGTGACACTGACTCCTGAGGAAGAGGCCC  
GCCTGAAGAAGAGCGCAGACACCCTCTGGGGAATCCAGAAGGAGCTGCAGTTCTAAA  
GTCTTCCCCGTGTCTAGCACTTCACTGTCCAGGCTGCAGCAGGGCTTCTAGGCAGA  
CCACACCCTTCTCGTCTGAGCTGTGGTTAGTACAGTGGTGTGAGATGGTGTGGGGA  
AACATCTCACTCCCCACAGCTCTGCCCTGCTGCCAAGTGGTACTTGTGTAGTGGTGA  
CCTGGTTAGTGTGACAGTCCCACTGTCTCTGAGACACACTGCCAACTGCAGGCTTCG  
ATTACCCCTGTGAGCCTGCTGCATTGCTGCCCTGCACCAAACAGCCTAGGCCGACGA  
GTTCCCAAGTTAAGTCGTATAACCTGGCTCCAGTGTGTACGTCCATGATGCATATCTT  
GTGCATAAATGTTGTACAGGATATTTTATATATTATATGTGTCTGTAGTGTGCATTG  
CAATATTATGTGAGATGTAAGATCTGCATATGGATGATGGAACCAACCACCCAAGTG  
TCATGCCAAATAAAACCTTGAACAGTG

*FIG. 12C*

MSKSSGGYTYTETSVLFFHFKVSKDSKSKMATLKDQLIVNLLKEEQAPQ  
NKITVVGVGAVGMACAISIIMKDLADELALVDVMEDKLKGEMMDLQHGS  
LFLKTPKIVSSKDYCVTANSKLVIIITAGARQQEGESRLNLVQRNVNIFK  
FIIIPNIVKYSPHCKLLIVSNPVDILTIVAWKISGFPKNRVIGSGCNLDS  
ARFRYLMGERLGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLKSLNP  
ELGTDADKEQWKEVHKQVVD SAYEVIK LKGYTSWAIGLSVADLAESIMK  
NLRRVHPISTMIKGLYGINEDVFLSVPCILGQNGISDVVKVTLTPEEEA  
RLKKSADTLWGIQKELQF

## FIG. 12D

CTCTGGTGTTTACTTGAGAAGCCCTGGCTGTGTCCTTGCTGTAGGAGCCGGAGTAG  
CTCAGAGTGATCTTGTCTGAGGAAAGGCCAGCCCCACTTGGTTAATAAACCGCGAT  
GGGTGAACCCTCAGGAGGCTATACTTACACCCAAACGTCGATATTCTTTTCCACG  
CTAAGATTCTTTTGGTTCCAAGTCCAATATGGCAACTCTAAAGGATCAGCTGATT  
TATAATCTTCTAAAGGAAGAACAGACCCCCCAGAATAAGATTACAGTTGTTGGGGT  
TGGTGCTGTTGGCATGGCCTGTGCCATCAGTATCTTAATGAAGGACTTGGCAGATG  
AACTTGCTCTTGTTGATGTCATCGAAGACAAATTGAAGGGAGAGATGATGGATCTC  
CAACATGGCAGCCTTTTCTTAGAACACCAAAGATTGTCTCTGGCAAAGACTATAA  
TGTAAGTCAAAGCTCCAAGCTGGTCATTATCACGGCTGGGGCACGTCAGCAAGAGG  
GAGAAAGCCGTCTTAATTTGGTCCAGCGTAACGTGAACATATTTAAATTCATCATT  
CCTAATGTTGTAAATAACAGCCCGAACTGCAAGTTGCTTATTGTTTCAAATCCAGT  
GGATATCTTGACCTACGTGGCTTGGAAGATAAGTGGTTTTCCCAAAAACCGTGTTA  
TTGGAAGTGGTTGCAATCTGGATTTCAGCCCGATTCCGTTACCTGATGGGGGAAAGG  
CTGGGAGTTACACCATTAAGCTGTCATGGGTGGGTCTTGGGGAACATGGAGATTC  
CAGTGTGCCTGTATGGAGTGGAATGAATGTTGCTGGTGTCTCTCTGAAGACTCTGC  
ACCCAGATTTAGGGACTGATAAAGATAAGGAACAGTGGAAGAGGTTTACAAGCAG  
GTGGTTGAGAGTGCTTATGAGGTGATCAAACCTCAAAGGCTACACATCCTGGGCTAT  
TGGACTCTCTGTAGCAGATTTGGCAGAGAGTATAATGAAGAATCTTAGGCGGGTGC  
ACCCAGTTTCCACCATGATTAAGGGTCTTTACGGAATAAAGGATGATGTCTTCCTT  
AGTGTTCCTTGCAATTTTGGGACAGAATGGAATCTCAGACCTTGTTGAAGGTGACTCT  
GACTTCTGAGGAAGAGGCCCGTTTGAAGAAGAGTGCAGATACACTTTGGGGGATCC  
AAAAGGAGCTGCAATTTTAAAGTCTTCTGATGTCATATCATTTCACTGTCTAGGCT  
ACAACAGGATTCTAGGTGGAGGTTGTGCATGTTGTCCTTTTTTATCTGATCTGTGAT  
TAAAGCAGTAATATTTTAAGATGGACTGGGAAAAACATCAACTCCTGAAGTTAGAA  
ATAAGAATGGTTTGTAAAATCCACAGCTATATCCTGATGCTGGATGGTATTAATCT  
TGTGTAGTCTTCAACTGGTTAGTGTGAAATAGTTCTGCCACCTCTGACGCACCACT  
GCCAATGCTGTACGTACTGCATTTGCCCTTGAGCCAGGTGGATGTTTACCGTGTG  
TTATATAACTTCTGGCTCCTTCACTGAACATGCCTAGTCCAACATTTTTTCCAG  
TGAGTCACATCCTGGGATCCAGTGTATAAATCCAATATCATGTCTTGTGCATAATT  
CTTCCAAAGGATCTTATTTTGTGAACATATCAGTAGTGACATTACCATATAATG  
TAAAAAGATCTACATACAAACAATGCAACCAACTATCCAAGTGTTATACCAACTAA  
AACCCCAATAAACCTTGAACAGTG

## FIG. 12E

**MGEPSGGYTYTQTSIFLFHAKIPFGSKSNMATLKDQLIYNLLKEEQTP**  
**QNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQH**  
**GSLFLRTPKIVSGKDYNVTANSKLVIIITAGARQQEGESRLNLVQRNVN**  
**IFKFIIPNVVKYSPNCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGC**  
**NLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGMNVAGVSL**  
**KTLHPDLGTDKDKKEQWKEVHKQVVESAYEVIKLGKGYTSWAIGLSVADL**  
**AESIMKNLRRVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVT**  
**LTSEEEARLKKSADTLWGIQKELQF**

**FIG. 12F**

CLUSTALW (V1.4) MULTIPLE SEQUENCE ALIGNMENT

3 SEQUENCES ALIGNED                      ALIGNMENT SCORE = 26102  
 GAPS INSERTED = 78                      CONSERVED IDENTITIES = 1013

PAIRWISE ALIGNMENT MODE: SLOW  
 PAIRWISE ALIGNMENT PARAMETERS:  
     OPEN GAP PENALTY = 10.0      EXTEND GAP PENALTY = 5.0

MULTIPLE ALIGNMENT PARAMETERS:  
     OPEN GAP PENALTY = 0.0      EXTEND GAP PENALTY = 5.0  
     DELAY DIVERGENT = 40%      TRANSITIONS: WEIGHTED

PROCESSING TIME: 8.7 SECONDS

RAT	1	CGCTC-TACTTGCTGT-AGGA-CTCTGG--GTGA--TGG	32
HUM	1	CTCTGGTGTTTACT-TGAGAAGCCCTGGCTGTGTCCTTG	38
MOU	1	GAGCAACTTGCGCTC-TACTTGCTGT-AGGG-CTCTGG--GTGA--TGG	43
		* * * * *	
RAT	33	GAG-AAGAGCGGGAGGGCAGTTCTT--TAACCGTGTAAGAGGAGGGACCA	79
HUM	39	CTGTAGGAGCCGGA--GTAGCTCAGAGTGATCTTGTCTGAGGAAAGGCCA	86
MOU	44	GAG-AAGAGCGGGAGGGCAGCTTTC--TAACCATATAAGAGGAGATACCA	90
		* * * * *	
RAT	80	TCCCT-TTTGG--GGTTCATCAAGATGAGTAAGAACTCAGGCGGCTACAC	126
HUM	87	GCCCCACTTGTTAATAAACCGCGATGGGTGAACCCTCAGGAGGCTATAC	136
MOU	91	TCCCC-TTTTG--G-TTCATCAAGATGAGTAAGTCCTCAGGCGGCTACAC	136
		*** * * * *	
RAT	127	ATATACGGAGACCTCAGTATTATTTTCCATTTCAGGTCCCAAAAGATT	176
HUM	137	TTACACCCAAACGTCGATATTCTTTTCCACGCTAAGATTCCTTTTGGTT	186
MOU	137	GTACACGGAGACCTCGGTATTATTTTCCATTTCAGGTCTCAAAAGATT	186
		* * * * *	
RAT	177	CAAAGTCCAAGATGGCAGCCCTCAAGGACCAGCTGATT-GTGAATCTTCT	225
HUM	187	CCAAGTCCAATATGGCAACTCTAAAGGATCAGCTGATTTAT-AATCTTCT	235
MOU	187	CAAAGTCCAAGATGGCAACCCTCAAGGACCAGCTGATT-GTGAATCTTCT	235
		* * * * *	
RAT	226	TAAGGAAGAACAGGTCCCCCAGAACAAGATTACAGTTGTTGGGGTTGGTG	275
HUM	236	AAAGGAAGAACAGACCCCCCAGAATAAGATTACAGTTGTTGGGGTTGGTG	285
MOU	236	TAAGGAAGAGCAGGCTCCCCCAGAACAAGATTACAGTTGTTGGGGTTGGTG	285
		*****	
RAT	276	CTGTTGGCATGGCTTGTGCCATCAGTATCTTAATGAAGGACTTGGCTGAT	325
HUM	286	CTGTTGGCATGGCTTGTGCCATCAGTATCTTAATGAAGGACTTGGCAGAT	335
MOU	286	CTGTTGGCATGGCTTGTGCCATCAGTATCTTAATGAAGGACTTGGCGGAT	335
		*****	

**FIG. 13A**

RAT	326	GAGCTTGCCCTTGTTGATGTCATAGAAGATAAGCTAAAGGGAGAGATGAT	375
HUM	336	GAACCTGCTCTTGTTGATGTCATCGAAGACAAATTGAAGGGAGAGATGAT	385
MOU	336	GAGCTTGCCCTTGTTGACGTCATGGAAGACAAACTCAAGGGCGAGATGAT	385
		** ***** ** * *****	
RAT	376	GGATCTTCAGCATGGCAGCCTTTTCCTTAAGACACCAAAAATTGTCTCCA	425
HUM	386	GGATCTCCAACATGGCAGCCTTTTCCTTAGAACACCAAAGATTGTCTCTG	435
MOU	386	GGATCTCCAGCATGGCAGCCTCTTCCTTAAACACCAAAAATTGTCTCCA	435
		***** ** *****	
RAT	426	GCAAAGATTATAGTGTGACTGCAAACCTCCAAGCTGGTCATTATCACCGCG	475
HUM	436	GCAAAGACTATAATGTAACCTGCAAACCTCCAAGCTGGTCATTATCACGGCT	485
MOU	436	GCAAAGACTACTGTGTAACCTGCGAACTCCAAGCTGGTCATTATCACCGCG	485
		***** ** *** *****	
RAT	476	GGGGCCCGTCAGCAAGAGGGAGAGAGCCGGCTCAATTTGGTCCAGCGAAA	525
HUM	486	GGGGCACGTGAGCAAGAGGGAGAAAGCCGTCTTAATTTGGTCCAGCGTAA	535
MOU	486	GGGGCCCGTCAGCAAGAGGGGGAGAGCCGGCTCAACCTGGTCCAGCGAAA	535
		***** ***** ** ***** ** *	
RAT	526	CGTGAACATCTTCAAGTTCATCATTCCAAATGTTGTGAAATACAGTCCAC	575
HUM	536	CGTGAACATATTTAAATTCATCATTCCTAATGTTGTAAAATACAGCCCGA	585
MOU	536	CGTGAACATCTTCAAGTTCATCATTCCTCAACATTTGTCAAGTACAGTCCAC	585
		***** ** ** ***** ** *****	
RAT	576	AGTGCAAACCTGCTCATCGTCTCAAACCCAGTGGATATCTTGACCTACGTG	625
HUM	586	ACTGCAAGTTGCTTATTGTTTCAAATCCAGTGGATATCTTGACCTACGTG	635
MOU	586	ACTGCAAGCTGCTGATCGTCTCCAATCCAGTGGATATCTTGACCTACGTG	635
		* ***** ** ** ** ** *****	
RAT	626	GCTTGGAAGATCAGCGGCTTCCCCAAAAACAAAGTTATTGGAAGTGGTTG	675
HUM	636	GCTTGGAAGATAAGTGGTTTTTCCCCAAAAACCGTGTTATTGGAAGTGGTTG	685
MOU	636	GCTTGGAATAATCAGTGGCTTTCCCCAAAAACCGAGTAATTGGAAGTGGTTG	685
		***** ** ** ** ***** ** *****	
RAT	676	CAATCTGGATTTCGGCTCGGTTCCGTTACCTGATGGGAGAAAGGCTGGGAG	725
HUM	686	CAATCTGGATTTCAGCCGATTCCGTTACCTGATGGGGGAAAGGCTGGGAG	735
MOU	686	CAATCTGGATTTCAGCGCGGTTCCGTTACCTGATGGGAGAGAGGCTGGGGG	735
		***** ** ** *****	
RAT	726	TTCATCCACTGAGCTGTCACGGGTGGGTCCTGGGAGAGCATGGCGACTCC	775
HUM	736	TTCACCCATTAAGCTGTCATGGGTGGGTCCTTGGGGAACATGGAGATTCC	785
MOU	736	TTCACGCGCTGAGCTGTCACGGCTGGGTCCTGGGAGAACATGGCGACTCC	785
		**** * ***** ** *****	
RAT	776	AGTGTGCCTGTGTGGAGTGGTGTGAACGTCGCCGGCGTCTCCCTGAAGTC	825
HUM	786	AGTGTGCCTGTATGGAGTGGAAATGAATGTTGCTGGTGTCTCTCTGAAGAC	835
MOU	786	AGTGTGCCTGTGTGGAGTGGTGTGAATGTTGCCGGCGTCTCCCTGAAGTC	835
		***** ***** ** ** ** *****	

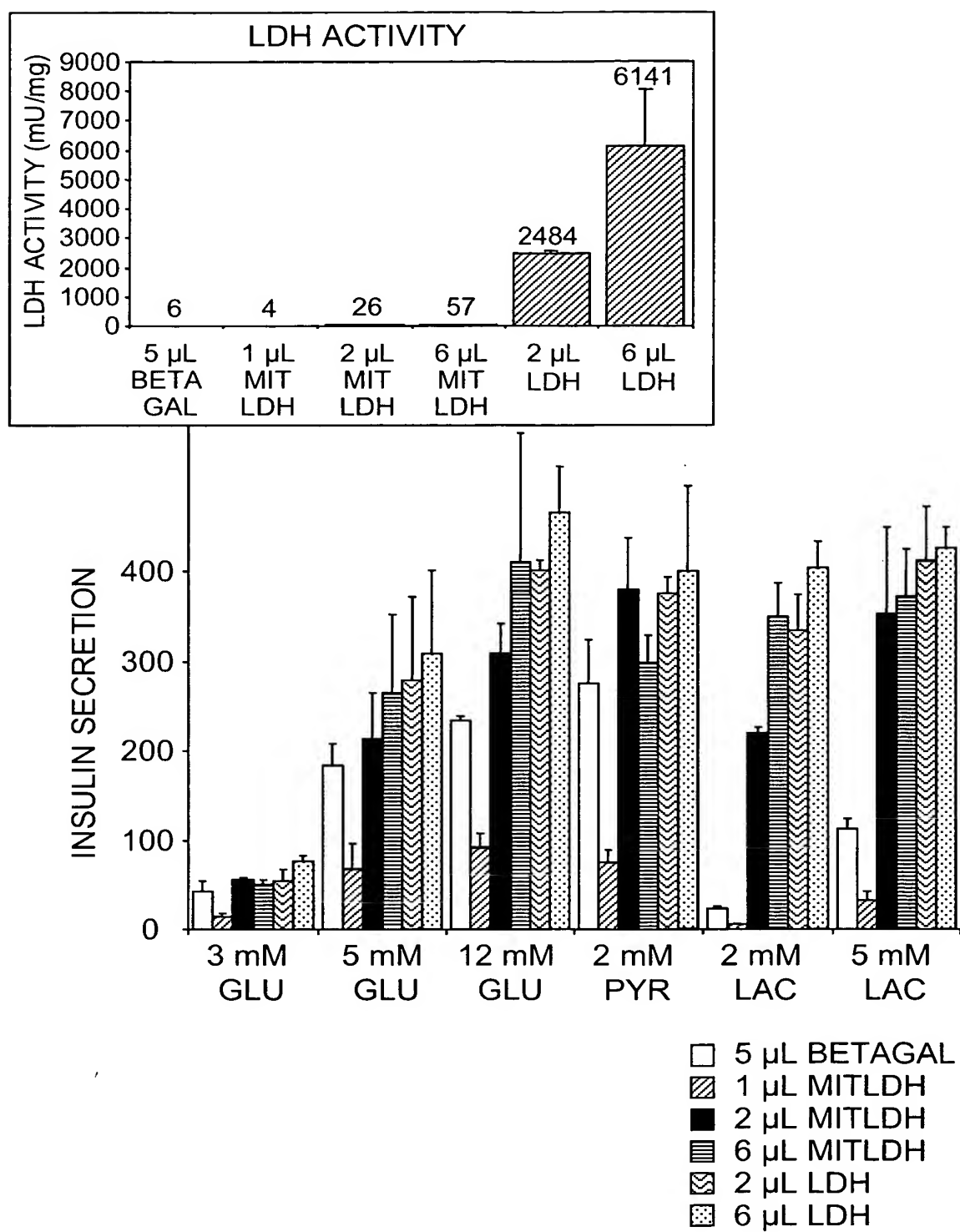
**FIG. 13B**

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RAT	826	TCTGAACCCGCAGCTGGGCACGGATGCAGACAAGGAGCAGTGGAAAGGATG	875
HUM	836	TCTGCACCCAGATTTAGGGACTGATAAAGATAAGGAACAGTGGAAAGAGG	885
MOU	836	TCTTAACCCAGAACTGGGCACCTGACGCAGACAAGGAGCAGTGGAAAGGAGG	885
		*** **	
RAT	876	TGCACAAGCAGGTGGTTGACAGTGCATACGAAGTGATCAAGCTGAAAGGT	925
HUM	886	TTCACAAGCAGGTGGTTGAGAGTGCTTATGAGGTGATCAAACTCAAAGGC	935
MOU	886	TTCACAAGCAGGTGGTTGGACAGTGCCTACGAGGTGATCAAGCTGAAAGGT	935
		* ****	
RAT	926	TACACATCCTGGGCCATTGGCCTCTCCGTGGCAGACTTGGCCGAGAGCAT	975
HUM	936	TACACATCCTGGGCTATTGGACTCTCTGTAGCAGATTTGGCAGAGAGTAT	985
MOU	936	TACACATCCTGGGCCATTGGCCTCTCTGTGGCAGACTTGGCTGAGAGCAT	985
		***** **	
RAT	976	AATGAAGAACCTTAGGCGGGTGATCCCA - TTTCCACCATGATTAAGGGT	1024
HUM	986	AATGAAGAATCTTAGGCGGGTGCA - CCCAGTTTCCACCATGATTAAGGGT	1034
MOU	986	AATGAAGAACCTTAGGCGGGTGATCCCA - TTTCCACCATGATTAAGGGT	1034
		*****	
RAT	1025	CTCTATGGGATCAAGGAGGATGTCTTCCTCAGCGTCCCATGTATCCTGGG	1074
HUM	1035	CTTTACGGAATAAAGGATGATGTCTTCCTTAGTGTTCTTGCATTTTGGG	1084
MOU	1035	CTCTATGGAATCAATGAGGATGTCTTCCTCAGTGTCCTCATGTATCCTGGG	1084
		** **	
RAT	1075	ACAAAATGGAATCTCAGATGTTGTGAAGGTGACACTGACTCCTGACGAGG	1124
HUM	1085	ACAGAATGGAATCTCAGACCTTGTGAAGGTGACTCTGACTTCTGAGGAAG	1134
MOU	1085	ACAAAATGGAATCTCGGATGTTGTGAAGGTGACACTGACTCCTGAGGAAG	1134
		*** ****	
RAT	1125	AGGCCCGCCTGAAGAAGAGTGCAGATACCCTCTGGGGAATCCAGAAGGAG	1174
HUM	1135	AGGCCCGTTTGAAGAAGAGTGCAGATACACTTTGGGGGATCCAAAAGGAG	1184
MOU	1135	AGGCCCGCCTGAAGAAGAGCGCAGACACCCTCTGGGGAATCCAGAAGGAG	1184
		*****	
RAT	1175	CTGCAGTTCTAAAGTCTTCCCAGTGTCTTAGCACTTCACTGTCCAGGCTG	1224
HUM	1185	CTGCAATTTTAAAGTCTTCT - GATGTCATATCATTTCACTGTCTAGGCTA	1233
MOU	1185	CTGCAGTTCTAAAGTCTTCCCCGTGTCCTAGCACTTCACTGTCCAGGCTG	1234
		*****	
RAT	1225	CAGCAGGGTTTCTA - -TGG-AGACCACGCAC-TT--C-TC-- -ATCTGAG	1264
HUM	1234	CAACAGGATT-CTAGGTGG-AGGTTGTGCATGTTGTCCTTTTATCTGAT	1281
MOU	1235	CAGCAGGGCTTCTA - -GGCAGACCACACCC-TT--C-TC-- -GTCTGAG	1274
		** ****	
RAT	1265	CTGTGGTTAGTCCAGTTG-GTCCAAAG	1290
HUM	1282	CTGTGATTAAAGCAGTAATATTTTAAAGATGGACTGGGAAAAACATCAACT	1331
MOU	1275	CTGTGGTTAGTACAGT-G-GTGTTGAGATGGTGTGGGGAAA-CAT-- -CT	1318
		*****	

RAT	1291		1290
HUM	1332	CCTGAAGTTAGAAATAAGAATGGTTTGTAATAATCCACAGCTATATCCTGA	1381
MOU	1319	C---A--CT-----C-----CCCACAGCTCTGCCCTGC	1341
RAT	1291		1290
HUM	1382	TGCTGGATGGTATTAATCTTGTGTAGTCTTCAACTGGTTAGTGTGAAATA	1431
MOU	1342	TGCCAAGTGG---TA--CTTGTGTAGTGGTGACCTGGTTAGTGTGA--CA	1384
RAT	1291		1290
HUM	1432	GTTCTGCCACCTCTGACGCACCACTGCCAATGCTGTACGTACTGCATTTG	1481
MOU	1385	GTCCCACTGTCTCTGAGACAC-ACTGCCAA--CTGCA-G-GCTTCGATTA	1429
RAT	1291		1290
HUM	1482	CCCCTTGAGCCAGGTGGATGTTTACCGTGTGTTATATAACTTCCTGGCTC	1531
MOU	1430	CCCCT-----G-TG-A-G----CC-TG--CTG--C-A-TTGCTG-C-C	1456
RAT	1291		1290
HUM	1532	CTTCACTGAACATGCCTAGTCCAACATTTTTTCCCAGT-GAGTCACATC-	1579
MOU	1457	CTGCACCAAACA-GCCTAGGCCGACGAGTT--CCCAGTTAAGTCGTATAA	1503
RAT	1291		1290
HUM	1580	CTGGGATCCAGTGTATAAATCCAATAT-CATGTCTTGTGCATAATTCTTC	1628
MOU	1504	CCTGGCTCCAGTGTGTACGTCCATGATGCATATCTTGTGCATAAATGTTG	1553
RAT	1291		1290
HUM	1629	CAAAGGATCTTATTT-TGTGAACTATATCAGTAGTGTACATTACCATATA	1677
MOU	1554	TACAGGATATTTTATATATTATATGTGTCTGTAGTGTGCATTGCAATATT	1603
RAT	1291		1290
HUM	1678	ATGTAA-A---AAGATCTACATACAAACAATGCAACCAACTATCCAAGTG	1723
MOU	1604	ATGTGAGATGTAAGATCTGCATATGGATGATGGAACCAACCACCAAGTG	1653
RAT	1291		1290
HUM	1724	TTATACCAACTAAAACCCCCAATAA-ACCTTGAACAGTG	1761
MOU	1654	TCATGCCAAATAAAACCTTGAACAGTG	1680





**FIG. 14**  
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